

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph from page 22, line 7 to page 23, line 8 with the following paragraph:

The major presence of *Candidatus* Endoecteinascidia frumentensis was confirmed by the analysis of the bacterial flora associated with the tunicate. To minimise the contribution of non-specifically associated bacteria contaminating the total DNA pool, tissue was cleaned as far as possible before DNA extraction. The incubation of live animals in sterile seawater helped to depurate (cleanse) the pharynx and gut of *E. turbinata*, which would have contained large numbers of non-specifically associated bacteria. Near full-length 16S rRNA gene fragments were amplified from the total DNA extracted from zooid, larval, stolon tissue and the control, scallop adductor muscle. After cloning and RFLP analysis, percentage dominance was assigned to the patterns observed in the three tissue types in order to determine any commonly occurring types. Four types were identified as occurring in all three tissue types and which also represented the most abundant RFLP types (see ~~Table 2~~ Table 1 and FIG. 1). The Type I pattern was the most common, representing between 42-67% of RFLP patterns observed in the three tissue types and the sequence analysis of this Type showed that it actually was *Candidatus* Endoecteinascidia frumentensis. Types VI, III and IV were the remaining three most abundant patterns (~~Table 2~~ Table 1, FIG. 1). The scallop control data showed no Type I (*Candidatus* Endoecteinascidia frumentensis), III or VI patterns, but a Type IV pattern was observed. This, together with the sequence analysis, identified Type IV as a commonly occurring marine-associated bacteria, and unlikely to have a specific relationship with *E turbinata*.

TABLE 2 TABLE 1

Dominance of RFLP patterns from zooid, larval and stolon material, and the total number of patterns observed.

RFLP Type (Pattern)	% dominance of RFLP types in <i>E. turbinata</i> tissue		
	ZOOID	LARVAE	STOLON
Type I (<i>Candidatus Endoecteinascidia frumentensis</i>)	42.6	55.9	67.0
Type III	5.6	9.6	5.3
Type IV	7.8	1.0	4.2
Type VI	14.6	4.3	10.0
Total number of clones digested	89	93	94
Total number of patterns observed	21	11	is

Please replace the paragraph at page 29, line 30 through page 30, line 4 with the following paragraph:

Probes were designed to putatively unique regions of the *Candidatus Endoecteinascidia frumentensis* and Type III 16S rDNA sequences:

TABLE 2

Oligonucleotide Sequences (5' - 3')	Application ^a	References
Symbiont specific		
EFRU-F1 CGG TAA CAT AAT AAA TGT TTT TTA CAT TTA TG	P, I, S	Herein
EFRU-R1 TAT GCT TTT GGG GAT TTG CTA GAT T	I, D, S	Herein

EFRU-R2	CTT TCG GTT ATC CTA GCC AC	I, D	Herein
Domain bacteria			
Type III-1	GCA ACT ATT TCT AGC TGT TAT TC	D	Herein
Type III-4	AGC TTT GCA CTG GAT GTC AAG	D	Herein
EUB338	GCT GCC TCC CGT AGG AGT	I, D	Amann et al., 1990
NON-EUB338	ACT CCT ACG GGA GGC AGC	I	Amann et al., 1990
EUB8-f	AG(AG) GTT TGA TC(AC) TGG CTC AG	P, S	Weiburg et al., 1999
EUB1509-r	G(GT)T ACC TTG TTA CGA CTT	P, S	Weiburg et al., 1999
16S-F1	GAG A(G/C)T TTG ATC (A/C/T)TG GCT CAG	P, S	Modified from Dorsch & Stackebrandt, 1992
1600R	AAG GAG GTG ATC CAG CC	P, S	Modified from Dorsch & Stackebrandt, 1992
Universal primers			
M13/pUC-f	GTT TTC CCA GTC ACG AC	S	
M13/ pUC-r	CAG GAA ACA GCT ATG AC	S	

*P = PCR primer; I = In situ hybridization probe; D = Dot-blot probe; S = Sequencing primers